

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/501,611  
Source: PCT  
Date Processed by STIC: 11/18/2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/501, 611

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos        was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will  
                                  prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers;  
     Numbering                use **space characters**, instead.
  
- 4      Non-ASCII              The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please**  
                                  **ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length        Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**  
                                  **each n or Xaa can only represent a single residue.** Please present the **maximum** number of each  
                                  residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0        A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                      sequences(s)             . Normally, PatentIn would automatically generate this section from the  
                                  previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                                  the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**  
                                  **Artificial or Unknown sequences.**
  
- 7      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
     (OLD RULES)              (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  This sequence is intentionally skipped  
  
                                  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences    Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
     (NEW RULES)              <210> sequence id number  
                                  <400> sequence id number  
                                  000
  
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)              Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                  In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10      Invalid <213>        Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or  
     Response                scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or  
                                  is Artificial Sequence
  
- 11      Use of <220>        ~~Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.~~  

Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or  
 "Unknown." Please explain source of genetic material in <220> to <223> section.  
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0        Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                                  listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa        "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



P  
PCT

## RAW SEQUENCE LISTING

DATE: 11/18/2005

PATENT APPLICATION: US/10/501,611

TIME: 10:51:29

Input Set : A:\-148-1.app

Output Set: N:\CRF4\11182005\J501611.raw

3 <110> APPLICANT: Pavan, William J.  
 4 Loftus, Stacie K.  
 5 The Government of the United States of America  
 6 as represented by The Secretary of the  
 7 Department of Health and Human Services  
 9 <120> TITLE OF INVENTION: Alteration of RAB38 Function to Modulate Mammalian  
 10 Pigmentation  
 12 <130> FILE REFERENCE: 015280-148100US  
 14 <140> CURRENT APPLICATION NUMBER: US 10/501,611  
 15 <141> CURRENT FILING DATE: 2004-07-14  
 17 <150> PRIOR APPLICATION NUMBER: US 60/349,929  
 18 <151> PRIOR FILING DATE: 2002-01-18  
 20 <150> PRIOR APPLICATION NUMBER: WO PCT/US03/01622  
 21 <151> PRIOR FILING DATE: 2003-01-17  
 23 <160> NUMBER OF SEQ ID NOS: 28  
 25 <170> SOFTWARE: PatentIn Ver. 2.1  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 8  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Mus musculus  
 32 <220> FEATURE:  
 33 <223> OTHER INFORMATION: Rab38 sequence of wildtype allele in C57Bl6/J +/-  
 34 DNA  
 36 <400> SEQUENCE: 1  
 37 ctgggtgt 8  
 40 <210> SEQ ID NO: 2  
 41 <211> LENGTH: 8  
 42 <212> TYPE: DNA  
 43 <213> ORGANISM: Mus musculus  
 45 <220> FEATURE:  
 46 <223> OTHER INFORMATION: Rab38 sequence of chocolate (cht) mutant allele in  
 47 c57Bl6/J Rab38cht/+ DNA  
 49 <400> SEQUENCE: 2  
 50 ctggktgt 8  
 53 <210> SEQ ID NO: 3  
 54 <211> LENGTH: 34  
 55 <212> TYPE: PRT  
 56 <213> ORGANISM: Homo sapiens  
 58 <220> FEATURE:  
 59 <223> OTHER INFORMATION: human RAB38 highly conserved N-terminal region  
 61 <400> SEQUENCE: 3  
 62 Met Gln Ala Pro His Lys Glu His Leu Tyr Lys Leu Leu Val Ile Gly  
 63 1 5 10 15

Does Not Comply  
 Corrected Diskette Needed  
 CP9-S)

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DATE: 11/18/2005

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TIME: 10:51:29

Input Set : A:\-148-1.app

Output Set: N:\CRF4\11182005\J501611.raw

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65 Asp Leu Gly Val Gly Lys Thr Ser Ile Ile Lys Arg Tyr Val His Gln
66          20          25          30
68 Asn Phe
71 <210> SEQ ID NO: 4
72 <211> LENGTH: 34
73 <212> TYPE: PRT
74 <213> ORGANISM: Rattus norvegicus
76 <220> FEATURE:
77 <223> OTHER INFORMATION: rat RAB38 highly conserved N-terminal region
79 <400> SEQUENCE: 4
80 Met Gln Thr Pro His Lys Glu His Leu Tyr Lys Leu Leu Val Ile Gly
81   1          5          10          15
83 Asp Leu Gly Val Gly Lys Thr Ser Ile Ile Lys Arg Tyr Val His Gln
84          20          25          30
86 Asn Phe
89 <210> SEQ ID NO: 5
90 <211> LENGTH: 34
91 <212> TYPE: PRT
92 <213> ORGANISM: Mus musculus
94 <220> FEATURE:
95 <223> OTHER INFORMATION: mouse RAB38 highly conserved N-terminal region
97 <400> SEQUENCE: 5
98 Met Gln Thr Pro His Lys Glu His Leu Tyr Lys Leu Leu Val Ile Gly
99   1          5          10          15
101 Asp Leu Gly Val Gly Lys Thr Ser Ile Ile Lys Arg Tyr Val His Gln
102          20          25          30
104 Asn Phe
107 <210> SEQ ID NO: 6
108 <211> LENGTH: 47
109 <212> TYPE: PRT
110 <213> ORGANISM: Homo sapiens
112 <220> FEATURE:
113 <223> OTHER INFORMATION: human RAB3a N-terminal region
115 <400> SEQUENCE: 6
116 Met Ala Ser Ala Thr Asp Ser Arg Tyr Gly Gln Lys Glu Ser Ser Asp
117   1          5          10          15
119 Gln Asn Phe Asp Tyr Met Phe Lys Ile Leu Ile Ile Gly Asn Ser Ser
120          20          25          30
122 Val Gly Lys Thr Ser Phe Leu Phe Arg Tyr Ala Asp Asp Ser Phe
123          35          40          45
126 <210> SEQ ID NO: 7
127 <211> LENGTH: 45
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <220> FEATURE:
132 <223> OTHER INFORMATION: human RAB5 N-terminal region
134 <400> SEQUENCE: 7
135 Met Ala Ser Arg Gly Ala Thr Arg Pro Asn Gly Pro Asn Thr Gly Asn
136   1          5          10          15

```

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Input Set : A:\-148-1.app

Output Set: N:\CRF4\11182005\J501611.raw

```

138 Lys Ile Cys Gln Phe Lys Leu Val Leu Leu Gly Glu Ser Ala Val Gly
139          20          25          30
141 Lys Ser Ser Leu Val Leu Arg Phe Val Lys Gly Gln Phe
142          35          40          45
145 <210> SEQ ID NO: 8
146 <211> LENGTH: 28
147 <212> TYPE: PRT
148 <213> ORGANISM: Homo sapiens
150 <220> FEATURE:
151 <223> OTHER INFORMATION: human N-RAS N-terminal region
153 <400> SEQUENCE: 8
154 Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
155 1          5          10          15
157 Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe
158          20          25
161 <210> SEQ ID NO: 9
162 <211> LENGTH: 1439
163 <212> TYPE: DNA
164 <213> ORGANISM: Homo sapiens
166 <220> FEATURE:
167 <223> OTHER INFORMATION: Rab38 cDNA
169 <400> SEQUENCE: 9
170 acatagagct cggggaacg tcgggtgccca gccccggctg tgcttcccag agcaagctcc 60
171 aggctccgca agaccgcgg gcctccagga tgcagacacc tcacaaggag cacctgtaca 120
172 agctgctggt gatcggcgac ctgggtgtgg gcaagaccag cattatcaag cgctatgtgc 180
173 accaaaactt ctctcgcac taccgggcca ccattggtgt ggacttcgcg ctgaagggtgc 240
174 tccactggga cccagagacg gtgggtgcgt tgcagctctg ggacattgct ggtcaagaaa 300
175 gatttggaag catgacaaga gtttattacc ggggaagctat gggggcattt attgtttttg 360
176 atgtcaccag accagccaca tttgaagccg tggcaaagtg gaaaaatgat ttggactcaa 420
177 agttaacgct ccctaattgt aagccagtgt cagtgttctt gttggccaac aaatgtgacc 480
178 aagggaagga tgtgcttatg aacaatggac tcaagatgga ccagttctgc aaggagcatg 540
179 gcttcgtagg atggtttgaa acatcagcca aggaaaacat aaacattgat gaagcctcaa 600
180 gatgcctggt caagcacata cttgcaaata agtgtgacct cctagagtct atagaaccgg 660
181 acattgtgaa gccccatctc acatcgccca aggttgtcag ctgctctggc tgtgccaaat 720
182 cctagaaggc tctctgctg gcatatgaca gacagaacct gtggccctca tgaatcgtgc 780
183 ttcagttttt ccttattacc attttgggta agcgtcagga tagggaagca catgtgacaa 840
184 gccaaagata catgactgta tggttcctgt caaagaggaa cagcaaattg tctttatgtg 900
185 ttttcccacc ccatcagcac agtggtttaca agcttttaaa atattagtct gtcacaatat 960
186 gctgttttat cattgagcaa agccactcag ggacacagac agccctaata tttgttcctt 1020
187 taaatcaaca aaggcttctg gtcttcttga gaaggggaat aacagagcaa ggcagaggtc 1080
188 aagctaagtg tggggatttg tcttgccctg gtgtgtcttt gttcaggtat caatttgttc 1140
189 ccgggtggtc tgataggtct attaaataga aaccattcat ggtagacctt agggttgkct 1200
190 gtgatgtttc tcttcagagt cgtgtgcaca ggcagcctgg gcttttgttg tcaattgctg 1260
191 tgccctgaat gctggtttta ctgaaaactg tatggaaaga tctgctccct gtatgtgcct 1320
192 ttctttcagc ttcctctgac tcaagctgca ggactcttct gtatgtggaa gatattattat 1380
193 atatattttt cacaagtga aaataaaaac ttaaaaatgc tgtttcctct tttctgata 1439
196 <210> SEQ ID NO: 10
197 <211> LENGTH: 291
198 <212> TYPE: DNA

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Input Set : A:\-148-1.app

Output Set: N:\CRF4\11182005\J501611.raw

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199 <213> ORGANISM: Homo sapiens
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Rab38 exon 1 and surrounding intron sequence
204 <400> SEQUENCE: 10
205 acatagagct cgggaaacg tcgggtgccca gccccggctg tgcttcccag agcaagctcc 60
206 aggctccgca agaccgcgg gcctccagga tgcagacacc tcacaaggag cacctgtaca 120
207 agctgctggt gatcggcgac ctgggtgtgg gcaagaccag cattatcaag cgctatgtgc 180
208 accaaaactt ctctcgcac taccgggcca ccattggtgt ggacttcgcg ctgaagggtgc 240
209 tccactggga cccagagacg gtgggtgcgt tgcagctctg ggacattgct g 291
212 <210> SEQ ID NO: 11
213 <211> LENGTH: 281
214 <212> TYPE: DNA
215 <213> ORGANISM: Homo sapiens
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Rab38 exon 2
220 <400> SEQUENCE: 11
221 gtcaagaaag atttggaac atgacaagag tttattaccg ggaagctatg ggggcattta 60
222 ttgtttttga tgtcaccaga ccagccacat ttgaagccgt ggcaaagtgg aaaaatgatt 120
223 tggactcaaa gttaacgctc cctaattgga agccagtgtc agtggttctg ttggccaaca 180
224 aatgtgacca agggaaggat gtgcttatga acaatggact caagatggac cagttctgca 240
225 aggagcatgg cttcgtagga tggtttgaaa catcagccaa g 281
228 <210> SEQ ID NO: 12
229 <211> LENGTH: 868
230 <212> TYPE: DNA
231 <213> ORGANISM: Homo sapiens
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Rab38 exon 3 and surrounding intron sequence
236 <400> SEQUENCE: 12
237 ggaaaacata aacattgatg aagcctcaag atgcctggtc aagcacatac ttgcaaata 60
238 gtgtgacctc ctagagtcta tagaacgga cattgtgaag ccccatctca catcgcccaa 120
239 ggttgtcagc tgctctggct gtgccaaatc ctagaaggct cctctgctgg catatgacag 180
240 acagaacccg tggccctcat gaatcgtgct tcagtttttc cttattacca ttttgggtaa 240
241 gcgtcaggat agggaagcac atgtgacaag ccaaagatac atgactgtat ggttcctgtc 300
242 aaagaggaac agcaaattgt ctttatgtgt tttcccacc catcagcaca gtgtttacaa 360
243 gcttttaaaa tattagtctg tcacaatatg ctgttttacc attgagcaaa gccactcagg 420
244 gacacagaca gccctaatat ttgttccttt aaatcaacaa aggcttctgg tcttcttgag 480
245 aaggggaata acagagcaag gcagagggtca agctaagtgt ggggatttgt cttgccctgg 540
246 tgtgtctttg ttcaggtatc aatttgttcc cgggtggtct gataggctca ttaaatagaa 600
247 accattcatg gtagacctaa gggttgkctg tgatgtttct cttcagagtc gtgtgcacag 660
248 gcagcctggg cttttgttgt cacttgctgt gccctgaatg ctggtttaac tgaaaactgt 720
249 atggaaagat ctgctccctg tatgtgcctt tctttcagct tctctgact caagctgcag 780
250 gactcttctg tatgtggaag atatattata tatatttttc acaagtgaag aataaaacat 840
251 taaaaatgct gtttcctgt ttctgata 868
254 <210> SEQ ID NO: 13
255 <211> LENGTH: 45
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence:TYRP15'T3F

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## RAW SEQUENCE LISTING

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Input Set : A:\-148-1.app

Output Set: N:\CRF4\11182005\J501611.raw

262 <400> SEQUENCE: 13  
 263 gcgcgaatta accctcacta aagggtctga gcaccctgt cttct  
 266 <210> SEQ ID NO: 14  
 267 <211> LENGTH: 45  
 268 <212> TYPE: DNA  
 269 <213> ORGANISM: Artificial Sequence  
 271 <220> FEATURE:  
 272 <223> OTHER INFORMATION: Description of Artificial Sequence: TYRP15'T7R  
 274 <400> SEQUENCE: 14  
 275 gcgcgtaata cgactcacta tagggccag ttgcaaaatt ccagt  
 278 <210> SEQ ID NO: 15  
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 280 <212> TYPE: DNA  
 281 <213> ORGANISM: Artificial Sequence  
 283 <220> FEATURE:  
 284 <223> OTHER INFORMATION: Description of Artificial Sequence: MLSN R T7  
 286 <400> SEQUENCE: 15  
 287 gcgggtaata cgactcacta tagggccac aaacatgtcc tacttac  
 290 <210> SEQ ID NO: 16  
 291 <211> LENGTH: 44  
 292 <212> TYPE: DNA  
 293 <213> ORGANISM: Artificial Sequence  
 295 <220> FEATURE:  
 296 <223> OTHER INFORMATION: Description of Artificial Sequence: MLSN FT3  
 298 <400> SEQUENCE: 16  
 299 gcgcgaatta accctcacta aagggaagct tccgactct ctac  
 302 <210> SEQ ID NO: 17  
 303 <211> LENGTH: 21  
 304 <212> TYPE: DNA  
 305 <213> ORGANISM: Artificial Sequence  
 307 <220> FEATURE:  
 308 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR  
 309 amplification primer Rab38 Ex1F  
 311 <400> SEQUENCE: 17  
 312 taggaaggag gattaaacc g  
 315 <210> SEQ ID NO: 18  
 316 <211> LENGTH: 21  
 317 <212> TYPE: DNA  
 318 <213> ORGANISM: Artificial Sequence  
 320 <220> FEATURE:  
 321 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR  
 322 amplification primer Rab38 Ex 1R  
 324 <400> SEQUENCE: 18  
 325 gaactcctca tggctcactc c  
 328 <210> SEQ ID NO: 19  
 329 <211> LENGTH: 26  
 330 <212> TYPE: DNA  
 331 <213> ORGANISM: Artificial Sequence  
 333 <220> FEATURE:

45

45

47

44

21

21

The type of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

Insufficient Response  
 What is the source  
 of genetic  
 material?  
 See glen #  
 10 on error  
 summary  
 sheet.

Same  
 Error.

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/501,611

DATE: 11/18/2005

TIME: 10:51:30

Input Set : A:\-148-1.app

Output Set: N:\CRF4\11182005\J501611.raw